

A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-552 <TA>
A;Cross-references: EMBL:U59446; NID:91655829; PID:AC08051.1; PID:91655830
A;Experimental source: cv. 20516 of Svalof's Karat; immature seed, 30 days after pollination

Query Match 12.3%; Score 119; DB 2; Length 552;
Best Local Similarity 30.2%; Pred. No. 0.15; Mismatches 55; Indels 56; Gaps 10;
Matches 51; Conservative 7; Mismatches 55; Indels 56; Gaps 10;

Qy 22 AECFDLLVRCVACGLIIRTPPKPAGASSPPAPTAQLOPQESVGAGAGEALPLPGLLFGA 81
Db 282 ADRIDALGAH---FGRPTTPAPRSPAPGPPAPA-----PGSHPAPAP----A 325

Qy 82 PARIGLALVALVLYLVGLVLSWRRRQRRLRGASSAEAPP-GDKDAPERPDKVILISPGIDA 140
Db 326 PA-----PGQGPRPAPAGPAGPRPSAP-----GPGPRPA 355

Qy 141 TAPAWPPGEGDCCTP--PG---HSVP--VPAELGSTELVLTTKTGP 181
356 PAPA-PAPGQGPRPAPGPPAPGCPHPPAPAARGTSATPAPAPMTKIGP 403

RESULT 3

EDBE23 immediate-early protein IER2.9 - bovine herpesvirus 1 (strain Jura)
N;Alternate name: early protein ER2.6; p135 protein
C;Species: bovine herpesvirus 1

C;Accession: JI-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 17-Mar-2000
C;Accession: B38209

R;Wirth, U.V.; Fraefel, C.; Vogt, B.; Vleek, C.; Paces, V.; Schwarzer, M.
J;Virol. 66, 2763-2772, 1992

A;Residues: 1-676 <WTR>
A;Cross references: GB:MR465; NID:9330769; PIDN:AA46062.1; PID:9330770
C;Superfamily: herpesvirus immediate-early protein IE10; RING finger homology
C;Keywords: DNA binding; immediate-early protein; transcription regulation; zinc finger
P;9-57/Domain: RING finger homology <RNG>
P;9-51/Region: zinc finger C3HC4 motif
P;284-331/Region: acidic

Query Match 12.1%; Score 116.5; DB 1; Length 676;
Best Local Similarity 30.4%; Pred. No. 0.27; Mismatches 78; Indels 51; Gaps 11;
Matches 62; Conservative 13; Mismatches 78; Indels 51; Gaps 11;

Db 7 SIRGRDAPAPTCVUPACFCDFDLVRYHCVACG-----LRTTPKPK 45
353 STRGRQTPAVQAPRPS-----LARR---PCGRRMAAVSAPPSSRSRGRRDPRLPAAPRAAP 405

Qy 46 AG---ASAPPRTALQPOQESVGAGBAAALPULGULGCAAPALLGLALVALVLVVG--LV 99
Db 406 AAQARACSSPEPR----SEGAGAGLGVVAGETAGTAGWAGGAGSEERGERHARLIGEAGPRVQ 460

Qy 100 SWMRQRRL-RGASSAEAPDGKDAPERPLDKVILSGISDATA-PAWPPGEGDPGTTP 157
Db 461 ARRRRRTFLDRAFTPAPAP--APAPARISTVIDL--ANAPRAPDAPAPAAARGASA 514

Qy 158 GHSVVPVPUPELGESTSLELYVTTKGP 181
Db 515 GAQITPA---AAAATTAANAP 534

RESULT 4

T46289 hypothetical protein DKFZp13A1010.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C;Accession: T46289
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gabberthuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000

A;Reference number: Z223035
A;Accession: T46289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-862 <AA>
A;Cross-references: EMBL:AL137579
A;Experimental source: adult testis; clone DKFZp13A1010
C;Genetics:
A;Note: DKFZp13A1010.1

Query Match 12.0%; Score 116; DB 2; Length 862;
Best Local Similarity 27.5%; Pred. No. 0.37; Mismatches 77; Indels 64; Gaps 11;
Matches 60; Conservative 17; Mismatches 77; Indels 64; Gaps 11;

Qy 10 GRDAP--APTRCPVAPBCFDLLVRYHCVACGLIIRTPR-KPAGASSPPRTALQPOSES--- 62
Db 328 GDPAPPSPAPSPAPASAAPPVR-----TPOAISPRPTSPASPAALDISPLAVS 377

Qy 63 -----VGAGAGEN-ALPUGLIGFG--APALGLALVALVLYVGIVSWSRRRQRNRG 110
Db 378 VPPAVLFLILGAGGAPASAATPPLSRSLPHLPLLKGAEAPLTDACQEMCSKLRG 437

Qy 111 ASSAEADGDKDAAPELDKVILSPLSGISDATAPAWPPGEGDP----- 152
Db 438 AQGPIGLPBMESPLLPP--PLSLRIG---GAP--PPPPRNPARMLALAQQVAEO 489

Qy 153 -----GTTTPGHSVPVP--ATELGSTELVLTTKTGP 181
Db 490 OSQQECGGTPPASQSPFHSLSLEVGGPLGTSGSCPP 527

RESULT 5

Gial growth factor - human
C;Species: Homo sapiens (man)

C;Accession: S22357
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2002

C;Accession: S22357
R;Marchionni, M.A.; Goodarl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; Henles, J.; Davis, J.B.; Hasan, J.J.; Totty, N.F.; Otsu, M.; McBurnie, R.N.; Waterfield, M.

A;Title: Gial growth factors are alternatively spliced erbB2 ligands expressed in the nervous system
A;Reference number: S32357; MUID:93205115; PMID:809607

A;Accession: S22357
A;Status: Preliminary

A;Molecule type: mRNA
A;Residues: 1-422 <WTR>

A;Cross references: GB:L12260; NID:9292047; PIDN:AB59622.1; PID:9292048
C;Superfamily: human heregulin; EGF homology

F;363-402/Domain: EGF homology <EGF>

Query Match 11.8%; Score 113.5; DB 2; Length 422;
Best Local Similarity 28.3%; Pred. No. 0.29; Mismatches 54; Conservative 15; Mismatches 51; Indels 71; Gaps 11;

Matches 54; Conservative 15; Mismatches 51; Indels 71; Gaps 11;

Db 2 RRGPRSRGRDAPAPTCVUPACFCDFDLVRYHCVACGLIIRTPR-KPAGASSP----- 51
4 RRAPRR-SGRSGP-----RAORPGSARSSPLPLPLLLL 38.

Qy 52 APRTALQPOQESVGAGBAAALPULGULGCAAPALLGLALVALVLVVGIVSWSRRRQR 106
Db 39 LGTAALAP---GAAAGNEAAPAGASVVCYSSPPSVGSVQHLAQRAVIEKGKVKHQRRQ 94

Qy 107 -----RUGGAGAEP--DGDKDAPSPLDKVILSPLSGISDATAPAWPPGEGDP-----GT 154
Db 95 GALDRKAANGAAGWGGIREPP-----AAGPRAIGPRAEPLLAANGT 139

RESULT 6

Qy 155 TPPGHSPVPA 165
Db 140 VPSWPTAPVPS 150

RESULT 6

T29018

Db	625 PKYQ 628
RESULT 8	
WJHU2H	homoeotic protein Hox B2 - human
N;Alternate names:	homeotic protein Hox 2.8; homeotic protein Hox 2H; homeotic protein
C;Species:	Homo sapiens (man)
C;Date:	30-Sep-1991 #sequence revision 30-Sep-1991 #text change 22-Jun-1999
C;Accession:	S07542; S00589; S15549; A56093; B37042; S404216
A;Molecule type:	DNA
A;Residues:	1-801 <KIR>
A;Cross-references:	EMBL:U23181; PIDN: AAC48204.1; GSPPDB:GN00020; CESP:ZK84.1
A;Experimental source:	strain Bristol N2; clone ZK84
A;Genetic:	
A;Gene:	CESP;ZK84.1
A;Map position:	2
A;Position:	22/2; 45/3; 108/1
C;Superfamily:	collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
Query Match	11.5%; Score 111; DB 2; Length 801;
Best Local Similarity	25.4%; Pred. No. 0.81; Mismatches 64; Indels 56; Gaps 8;
Matches	45; Conservative 12; Mismatches 64; Indels 56; Gaps 8;
Qy	12 DAPAPTCUPAECDDLLVRLRHCVACGLLRPRPKPGASSPAPRA-LQPOESVGAGAEA 70
Db	405 DTPPAPAAE-----TPAPAPAEERPAPEAASAPPAGGAPADY 448
Qy	71 ALPLFLGLLFGAPALIGLALVLALVLYGLVSWRRRQLRGASSAARPDKDAP-EPLDK 129
Db	449 AAP-ADVATTAPE-----TSSACGSAAGSYDVISSEPASE 480
Qy	130 VII----LSPGISDATAPAWPPCGDPGTTPPGHSSVPVATELGSTELVTIKTAGP 181
Db	481 VTAPIVSETEAPSDAAPIGPAASE-PAPAP---IEAPATDAATLETPAPAAEP 532
RESULT 7	
B35098	MC class III histocompatibility antigen HLA-B-associated protein 2 [imported] - human
C;Species:	Homo sapiens (man)
C;Date:	10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 24-Aug-2001
C;Accession:	B35098
R;Banerji, J.; Sands, J.; Strominger, J.L.; Spiess, T.	Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990
A;Title:	A gene pair from the human major histocompatibility complex encodes large proline-rich proteins.
A;Reference number:	A35098; MUID:90192810; PMID:2156268
A;Accession:	B35098
STATUS: preliminary	
;Molecule type: mRNA	
;Residues: 1-2142 <BAN>	
A;Cross-references:	GB:M33509; NID:9179338; PIDN:AAA35585.1; PIDN:9179339; GB:M31293
A;Note:	the authors translated the codon AGT for residue 97 as Gly
C;Superfamily:	collagen alpha 1(IV) chain
Query Match	11.1%; Score 107; DB 2; Length 2142;
Best Local Similarity	25.0%; Pred. No. 4; Mismatches 48; Indels 74; Gaps 10;
Matches	46; Conservative 16; Mismatches 48; Indels 74; Gaps 10;
Qy	14 PAPPCPVCAPECDFDLVLRHVACGKLRTPPKPGASSPAPTAQPOQESVGAGAGAAALP 73
Db	506 PAPPPAVPK-----LPAP-PAPPPRSAPTPET-EPEPEAQAPPROST-P 547
Qy	74 LPGILFLGAPALLGLGLALVLVGLVSWRRRQLRGASSAEEPQG-----DK 121
Db	548 TPGVA-AATPLVS-----GGGSSTSSGSPEASPVERQLPSK 584
Qy	122 DAPPPDLKYLILSPGGSIDATAPAWNPPIGDPPGTTPGHSVPVATELGSTELVTIKTAG- 180
Db	585 EGPPFPPEEV-----PPP-----TIPPVVKVEPKGKGIGPTRQPSSQGLY 624
Qy	181 PEQQ 184
Quary Match	11.0%; Score 106.5; DB 1; Length 356;
Best Local Similarity	24.7%; Pred. No. 0.81; Mismatches 66; Indels 89; Gaps 12;
Matches	56; Conservative 16; Mismatches 66; Indels 89; Gaps 12;
Qy	5 PRS-LGRDRAFTA---PTPCUPAECDDLLVRLRHCVACGLLRPRP-----KPA- 46
Db	66 PRSQRKAEDGFLUPPPPPRPPA-----APAPAPERFWMKKKSAKKPSQ 109
Qy	47 GASPPAPTAQPOQESVGAGAEAALPLPG-----IL-----FG 80
Db	110 SATPSPPAASKVAPVAGSGVSPADGLGLPEAGGGARRRTAYNTQOLLELEKFHFNKYLC 169
Qy	81 APALLGLALVAVLVGVSN-----RRQRRLRGASSAEPDKDABPFLDKV-----I 132

Db 170 RPRVEIAALDLITERQKVWFONRMRKHKRQTOHREPPDGPACPGALEIDCDPAEPA 229
 Qy 133 LSPGISDATAPAW----PP---PG-----EDPPTPPG 158
 Db 230 ASPGGPSASRAWEACCHPPEVPGALSADPRPLAVRLLEGAGASSPG 276

A;Experimental source: strain Sprague Dawley; brain
 C;Function:
 A;Description: may be involved in cytomatrix organization at the site of neurotransmitter
 A;Note: component of the presynaptic cytoskeleton
 C;Keywords: coiled coil; zinc finger

RESULT 9
 A55558 albumin D-box binding protein - human
 C;Species: Homo sapiens (man)
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 01-Dec-2000
 C;Accession: A55558; GO2887; #sequence_revision 18-Aug-1995 #text_change 01-Dec-2000
 R;Khatib, Z. A.; Inaba, T.; Valentine, M.; Look, A.T.
 Genomics 23, 344-351, 1994
 A;Title: Chromosomal localization and cDNA cloning of the human DBP and TEP genes.
 A;Reference number: A55558; MUID:95137580; PMID:7835883
 A;Accession: A55558
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: GB:U06936; NID:9606798; PIDN:AAA81374.1; PID:9606799
 R;Mueller, C.R.
 Submitted to the EMBL Data Library, February 1996
 A;Reference number: H01797
 A;Accession: G02887
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-178; 'S', 180-325 <MUE>
 C;Genetics:
 A;Gene: GDB:DBP
 A;Cross-references: GDB:128840; OMIM:124097
 A;Map position: 4q12-4q12
 A;Introns: 47/1; 184/1; 254/3

Query Match 10.8%; Score 104.5; DB 2; Length 3938;
 Best Local Similarity 26.8%; Pred. No. 11; Mismatches 73; Indels 59; Gaps 10;
 Matches 53; Conservative 13; MisMatches 73; Indels 59; Gaps 10;
 Query Match 10.8%; Score 104.5; DB 2; Length 3938;
 Best Local Similarity 26.8%; Pred. No. 11; Mismatches 73; Indels 59; Gaps 10;
 Matches 53; Conservative 13; MisMatches 73; Indels 59; Gaps 10;
 C;Species: human herpesvirus 4, Epstein-Barr virus
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Jan-2000
 C;Accession: S27923
 R;Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Farrell, P.J.
 Submitted to the EMBL Data Library, August 1990
 A;Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B9
 A;Reference number: S27923
 A;Accession: S27923
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-324 <PR>
 A;Cross-references: EMBL:M35547; NID:9330420; PIDN:AAA45896.1; PID:9330421
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 Query Match 10.7%; Score 103.5; DB 2; Length 924;
 Best Local Similarity 28.6%; Pred. No. 3.3.; Mismatches 68; Indels 53; Gaps 9;
 Matches 54; Conservative 14; Mismatches 68; Indels 53; Gaps 9;
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 21-Apr-1998 #sequence_revision 01-May-1998 #text_change 05-Nov-1999
 C;Accession: S72273
 A;Molecule type: mRNA
 A;Cross-references: EMBL:Y16563; NID:93413503; PIDN:CAA76287.1; PID:93413504

RESULT 10
 Bassoon protein - rat
 N;Alternate name: brain-specific synapse-associated protein
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C;Accession: T42761
 R;Dick, S.; Samant-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Mex,
 J. Cell Biol. 142, 459-509, 1998
 A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
 A;Reference number: 222249; MUID:98345363; PMID:9679147
 A;Accession: T42761
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Residue: I-3338 <DE>
 A;Cross-references: EMBL:Y16563; NID:93413503; PIDN:CAA76287.1; PID:93413504

RESULT 11
 S27923 gene LF3 protein - human herpesvirus 4
 C;Species: human herpesvirus 4, Epstein-Barr virus
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Jan-2000
 C;Accession: S27923
 R;Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Farrell, P.J.
 Submitted to the EMBL Data Library, August 1990
 A;Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B9
 A;Reference number: S27923
 A;Accession: S27923
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-324 <PR>
 A;Cross-references: EMBL:M35547; NID:9330420; PIDN:AAA45896.1; PID:9330421
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 Query Match 10.7%; Score 103.5; DB 2; Length 924;
 Best Local Similarity 28.6%; Pred. No. 3.3.; Mismatches 68; Indels 53; Gaps 9;
 Matches 54; Conservative 14; Mismatches 68; Indels 53; Gaps 9;
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 21-Apr-1998 #sequence_revision 01-May-1998 #text_change 05-Nov-1999
 C;Accession: S72273
 A;Molecule type: mRNA
 A;Cross-references: EMBL:Y16563; NID:93413503; PIDN:CAA76287.1; PID:93413504

RESULT 12
 S72273 actin-depolymerizing protein N-WASP, brain - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 21-Apr-1998 #sequence_revision 01-May-1998 #text_change 05-Nov-1999
 C;Accession: S72273
 R;Miki, H.; Miura, K.; Takenawa, T.
 EMBO J. 15, 5326-5335, 1996
 Query Match 10.8%; Score 104.5; DB 2; Length 3938;
 Best Local Similarity 26.8%; Pred. No. 11; Mismatches 73; Indels 59; Gaps 10;
 Matches 53; Conservative 13; MisMatches 73; Indels 59; Gaps 10;
 Query Match 10.8%; Score 104.5; DB 2; Length 3938;
 Best Local Similarity 26.8%; Pred. No. 11; Mismatches 73; Indels 59; Gaps 10;
 Matches 53; Conservative 13; MisMatches 73; Indels 59; Gaps 10;
 C;Species: human herpesvirus 4, Epstein-Barr virus
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Jan-2000
 C;Accession: S27923
 R;Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Farrell, P.J.
 Submitted to the EMBL Data Library, August 1990
 A;Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B9
 A;Reference number: S27923
 A;Accession: S27923
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-324 <PR>
 A;Cross-references: EMBL:M35547; NID:9330420; PIDN:AAA45896.1; PID:9330421
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
 Query Match 10.7%; Score 103.5; DB 2; Length 924;
 Best Local Similarity 28.6%; Pred. No. 3.3.; Mismatches 68; Indels 53; Gaps 9;
 Matches 54; Conservative 14; Mismatches 68; Indels 53; Gaps 9;
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 21-Apr-1998 #sequence_revision 01-May-1998 #text_change 05-Nov-1999
 C;Accession: S72273
 A;Molecule type: mRNA
 A;Cross-references: EMBL:Y16563; NID:93413503; PIDN:CAA76287.1; PID:93413504

A;Title: N-WASP, a novel actin-depolymerizing protein, regulates the cortical cytoskeleton

A;Reference: S72273; MUID:97050838; PMID:8895577

A;Accession: S72273

A;Status: nucleic acid sequence not shown

A;Molecule type: RNA

A;Residues: 1-505 <MIK>

A;Cross-references: EMBL:D67066; NID:91644231; PIDN:BA11082.1; PID:d1011742; PID:916442

A;Experimental source: brain

Query Match 10.7%; Score 103; DB 2; Length 505;
Best Local Similarity 23.6%; Pred. No. 2; Gaps 7;
Matches 41; Conservative 4; Mismatches 45; Indels 84; Gaps 7;

```

QY  5 PRSLRGDQAPATC-VPAECFDLVLVRHCVACGLRTPRKPA---GASSPAPRTALQ 59
Db  301 PPPARGRGAPPPPSRAPTA-----PPPPPSREGVGAAPPPPRMYP 345
QY  60 QESVAGAGAEEALIIPGLGAPALIGLALVLALVLUVGLVSWRQRRLGASSAEPDG 119
Db  346 -----DPLA-----PSSAPSG 357

```

120 DKQARPEPDKVILISPGISDATAAPAWPQGEDRGTTP-----GHSVPVPA 165
358 PPPPPPL-----SVGSVAVPPPPPPCPPPPGLPSGDHQVTPA 403

Db 1868 --SQQHQTGQAPAOQRPQAQAPATPTITSAPPRTTLLAPPPPPPPEDPP 1925

QY 155 TPPGHISVPVPA 165
Db 1926 PPP---PPPA 1932

RESULT 13

T38236 hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T38236

C;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, February 1998

A;Reference number: Z21780

A;Accession: T38236

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residue: 1-1611 <MR>

A;Cross-references: EMBL:AL021813; PIDN:CAN169911; GSPDB:CN00066; SPDB:SPAC23A1.17

A;Experimental source: strain 972h-; cosmid c23A1.

A;Genetic: SPDB:SPAC23A1.17

A;Map position: 1

Query Match 10.7%; Score 103; DB 2; Length 1611;
Best Local Similarity 24.6%; Pred. No. 6; Gaps 7;
Matches 44; Conservative 16; Mismatches 71; Indels 48; Gaps 7;

```

QY  13 APAPTCAECFDLVLVRHCVACGLRTPRKPAQGASSPAPRTALQPOESVAGAGEAL 72
Db  1078 APSPGAPPVPA-----PSGPDPVPKPSVAAPVPKPSVAVPP--VPAPSGAPPV 1123
QY  73 PLRGLI-----FGCAPALIGLALVLVNLVGLVSWRRQRRLGASSAEPDGKDAPF 125
Db  1124 PKPSVAAVVPPVPPGAPPV-----PKPSVAAVVPPGAPSG--Ap- 1159
QY  126 PLDKVTLISPGI--SDATAPAWPWPQGEDPDTTPGHSVVPATELGSTLVTTKTAGP 181
Db  1160 PVPKESVAAAPVPPVPAASSGIPPPKPEAAGYVPPVPPSEAPPVVKPSVGVPPVPPSTAPP 1218

```

RESULT 14

T48814 hypothetical protein 15B6.220 [imported] - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000

C;Accession: T48814

R.Schulte, U.; Aigr, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, A.; Reference number: Z24541

A;Accession: T48814

A;Status: preliminary

Query Match 10.7%; Score 103; DB 2; Length 1952;
Best Local Similarity 29.0%; Pred. No. 7.2; Gaps 4;
Matches 38; Conservative 15; Mismatches 62; Indels 16; Gaps 4;

```

QY  41 PRPKAGASSBAPRTALQ-QESVAGAGAEGALPLGLGAPALIGLALVLVLUVGLV 99
Db  1812 PAPSAAQSVPVAPVSSTPVPAVATVAPASTVVAAPTRVTPAALISAATVPAPV---- 1867
QY  100 SWRRQRRLGASSAEPDGKDABEPLDKVILS----PGISDATAAPAWPPPSDPPGT 154
Db  1868 --SQQHQTGQAPAOQRPQAQAPATPTITSAPPRTTLLAPPPPPPPEDPP 1925

```

QY 155 TPPGHISVPVPA 165
Db 1926 PPP---PPPA 1932

RESULT 15

S55659 tegument protein 64 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999

C;Accession: S55659

R.Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MUID:95302501; PMID:7783207

A;Accession: S55659

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residue: 1-13436 <TEL>

A;Cross-references: GB:U20824; NID:9695172; PIDN: AAC11852.1; PID:9695237

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1999.

Query Match 10.7%; Score 103; DB 2; Length 3436;
Best Local Similarity 25.0%; Pred. No. 12; Gaps 11;
Matches 55; Conservative 12; Mismatches 51; Indels 102; Gaps 11;

```

QY  2 RRGPSLRLGRD-----APAT-----PCVPAECFDL-----VRHCVAC 35
Db  3178 RLGERGRREEVVEAVAPAPDYSRPRVPRPREGPGRPRPARDTIGGAGSRKVE 3237
QY  36 G-----LARTRPRKGAGASSPAPRTALQPOESVAGAGAEGALPLGLGAPALIGL 88
Db  3238 GRGRPRVQLRSRSPKRPAASQVQGER-----EEVGFSPGKAR----- 3274

```

QY 89 LVLAIVLVLVGLVSWRQRRLGASSAEPDGKDAPFLPLKVLISPL----- 135
Db 3275 -----RGGSTAH-----PB-TDADYIEPPKSCVGAGSGPPE 3307

QY 136 -----GISDATAPAWPWPQGEDPDTTPGHSVVPATELGSTLVTTKTAGP 171
Db 3308 KKQGQAAEAAPA-PREGEQAAERGEPEGTTPBPS-IGKT 3345

Search completed: June 23, 2003, 15:16:43
Job time : 49 secs

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